SEQUENCE LISTING

<110> Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH

<120> Vaccine against Oncovirus Infections, such as infections by Feline leukosis virus of the cat

<130> XI 1292-03

<150> DE 102 44 863.9
<151> 2002-09-23

<160> 40

<170> PatentIn version 3.3

<210> 1
<211> 1929
<212> DNA
<213> Feline leukemia virus

<220>
<221> gene
<222> (1)..(1929)
<223> DNA sequence wild type "env" gene without signal peptide coding region

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<210> 2
<211> 1527
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<213> Feline leukemia virus

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<221> gene
<222> (1)..(1527)
<223> DNA sequence wild type "gag" gene

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gccgaatggg taatgatgaa tgtaggttgg ccccgagaag gaactttcac cattgacaat 180

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<210> 3
<211> 642
<212> PRT
<213> Feline leukemia virus

<220>
<221> PEPTIDE
<222> (1)..(447)
<223> Amino acid sequence of the protein corresponding to Seq.ID1

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Trp Asn Leu Ala Phe Leu Val Gly Ile Leu Phe Thr Ile Asp Ile Gly
20 25 30

Met Ala Asn Pro Ser Pro His Gln Ile Tyr Asn Val Thr Trp Val Ile
35 40 45

Thr Asn Val Gln Thr Asn Thr Gln Ala Asn Ala Thr Ser Met Leu Gly
50 55 60

Thr Leu Thr Asp Ala Tyr Pro Thr Leu His Val Asp Leu Cys Asp Leu
65 70 75 80

Val Gly Asp Thr Trp Glu Pro Ile Val Leu Asn Pro Thr Asn Val Lys
85 90 95

His Gly Ala Arg Tyr Ser Ser Ser Lys Tyr Gly Cys Lys Thr Thr Asp
100 105 110

Arg Lys Lys Gln Gln Gln Thr Tyr Pro Phe Tyr Val Cys Pro Gly His
115 120 125

Ala Pro Ser Leu Gly Pro Lys Gly Thr His Cys Gly Gly Ala Gln Asp
130 135 140

Gly Phe Cys Ala Ala Trp Gly Cys Glu Thr Thr Gly Glu Ala Trp Trp
145 150 155 160

Lys Pro Thr Ser Ser Trp Asp Tyr Ile Thr Val Lys Arg Gly Ser Ser
165 170 175

Gln Asp Asn Ser Cys Glu Gly Lys Cys Asn Pro Leu Val Leu Gln Phe
180 185 190

Thr Gln Lys Gly Arg Gln Ala Ser Trp Asp Gly Pro Lys Met Trp Gly

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        195                 200                 205

Leu Arg Leu Tyr Arg Thr Gly Tyr Asp Pro Ile Ala Leu Phe Thr Val
    210                 215                 220

Ser Arg Gln Val Ser Thr Ile Thr Pro Pro Gln Ala Met Gly Pro Asn
225                 230                 235                 240

Leu Val Leu Pro Asp Gln Lys Pro Pro Ser Arg Gln Ser Gln Thr Gly
                245                 250                 255

Ser Lys Val Ala Thr Gln Arg Pro Gln Thr Asn Glu Ser Ala Pro Arg
            260                 265                 270

Ser Val Ala Pro Thr Thr Met Gly Pro Lys Arg Ile Gly Thr Gly Asp
        275                 280                 285

Arg Leu Ile Asn Leu Val Gln Gly Thr Tyr Leu Ala Leu Asn Ala Thr
    290                 295                 300

Asp Pro Asn Lys Thr Lys Asp Cys Trp Leu Cys Leu Val Ser Arg Pro
305                 310                 315                 320

Pro Tyr Tyr Glu Gly Ile Ala Ile Leu Gly Asn Tyr Ser Asn Gln Thr
                325                 330                 335

Asn Pro Pro Pro Ser Cys Leu Ser Thr Pro Gln His Lys Leu Thr Ile
            340                 345                 350

Ser Glu Val Ser Gly Gln Gly Met Cys Ile Gly Thr Val Pro Lys Thr
        355                 360                 365

His Gln Ala Leu Cys Asn Lys Thr Gln Gln Gly His Thr Gly Ala His
    370                 375                 380

Tyr Leu Ala Ala Pro Asn Gly Thr Tyr Trp Ala Cys Asn Thr Gly Leu
385                 390                 395                 400

Thr Pro Cys Ile Ser Met Ala Val Leu Asn Trp Thr Ser Asp Phe Cys
                405                 410                 415

Val Leu Ile Glu Leu Trp Pro Arg Val Thr Tyr His Gln Pro Glu Tyr
            420                 425                 430
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Val Tyr Thr His Phe Ala Lys Ala Val Arg Phe Arg Arg Glu Pro Ile
        435                 440                 445

Ser Leu Thr Val Ala Leu Met Leu Gly Gly Leu Thr Val Gly Gly Ile
    450                 455                 460

Ala Ala Gly Val Gly Thr Gly Thr Lys Ala Leu Leu Glu Thr Ala Gln
465                 470                 475                 480

Phe Arg Gln Leu Gln Met Ala Met His Thr Asp Ile Gln Ala Leu Glu
                485                 490                 495

Glu Ser Ile Ser Ala Leu Glu Lys Ser Leu Thr Ser Leu Ser Glu Val
            500                 505                 510

Val Leu Gln Asn Arg Arg Gly Leu Asp Ile Leu Phe Leu Gln Glu Gly
        515                 520                 525

Gly Leu Cys Ala Ala Leu Lys Glu Glu Cys Cys Phe Tyr Ala Asp His
    530                 535                 540

Thr Gly Leu Val Arg Asp Asn Met Ala Lys Leu Arg Glu Arg Leu Lys
545                 550                 555                 560

Gln Arg Gln Gln Leu Phe Asp Ser Gln Gln Gly Trp Phe Glu Gly Trp
                565                 570                 575

Phe Asn Lys Ser Pro Trp Phe Thr Thr Leu Ile Ser Ser Ile Met Gly
            580                 585                 590

Pro Leu Leu Ile Leu Leu Leu Ile Leu Leu Phe Gly Pro Cys Ile Leu
        595                 600                 605

Asn Arg Leu Val Gln Phe Val Lys Asp Arg Ile Ser Val Val Gln Ala
    610                 615                 620

Leu Ile Leu Thr Gln Gln Tyr Gln Gln Ile Lys Gln Tyr Asp Pro Asp
625                 630                 635                 640

Arg Pro
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<210> 4
<211> 508
<212> PRT
<213> Feline leukemia virus

<220>
<221> PEPTIDE
<222> (1)..(508)
<223> Amino acid sequence of the protein corresponding to Seq.ID2

<400> 4

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Met Gly Gln Thr Ile Thr Thr Pro Leu Ser Leu Thr Leu Asn His Trp
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Ser Glu Val Gln Ala Arg Ala Arg Asn Gln Gly Val Glu Val Arg Lys
            20                  25                  30

Lys Lys Trp Ile Thr Leu Cys Glu Ala Glu Trp Val Met Met Asn Val
        35                  40                  45

Gly Trp Pro Arg Glu Gly Thr Phe Thr Ile Asp Asn Ile Ser Gln Val
    50                  55                  60

Glu Glu Arg Ile Phe Ala Pro Gly Pro Tyr Gly His Pro Asp Gln Ile
65                  70                  75                  80

Pro Tyr Ile Thr Thr Trp Arg Ser Leu Ala Thr Asp Pro Pro Pro Trp
                85                  90                  95

Val Arg Pro Phe Leu Pro Pro Pro Lys His Pro Arg Thr Asp Pro Pro
            100                 105                 110

Glu Pro Leu Ser Pro Gln Pro Leu Ala Pro Gln Pro Ser Ser Pro His
        115                 120                 125

Pro Val Leu Tyr Pro Val Leu Pro Lys Pro Asp Pro Pro Lys Ala Pro
    130                 135                 140

Val Leu Pro Pro Asn Pro Ser Ser Pro Leu Ile Asp Leu Leu Thr Glu
145                 150                 155                 160

Glu Pro Pro Pro Tyr Pro Gly Gly His Gly Pro Thr Pro Pro Ser Gly
                165                 170                 175
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Pro Arg Thr Pro Thr Ala Ser Pro Ile Ala Ile Arg Leu Arg Glu Arg
            180                 185                 190

Arg Glu Asn Pro Ala Glu Lys Ser Gln Ala Leu Pro Leu Arg Glu Asp
        195                 200                 205

Pro Asn Asn Arg Pro Gln Tyr Trp Pro Phe Ser Ala Ser Asp Leu Tyr
    210                 215                 220

Asn Trp Lys Leu His Asn Pro Pro Phe Ser Gln Asp Pro Val Ala Leu
225                 230                 235                 240

Thr Asn Leu Ile Glu Ser Ile Leu Val Thr His Gln Pro Thr Trp Asp
                245                 250                 255

Asp Cys Gln Gln Leu Leu Gln Ala Leu Leu Thr Ala Glu Glu Arg Gln
            260                 265                 270

Arg Val Leu Leu Glu Ala Arg Lys Gln Val Pro Gly Glu Asp Gly Arg
        275                 280                 285

Pro Thr Gln Leu Pro Asn Val Val Asp Glu Ala Phe Pro Leu Thr Arg
    290                 295                 300

Pro Asn Trp Asp Phe Cys Thr Pro Ala Gly Arg Glu His Leu Arg Leu
305                 310                 315                 320

Tyr Arg Gln Leu Leu Leu Ala Gly Leu Arg Gly Ala Ala Arg Arg Pro
                325                 330                 335

Thr Asn Leu Ala Gln Val Lys Gln Val Val Gln Gly Lys Glu Glu Thr
            340                 345                 350

Pro Ala Ser Phe Leu Glu Arg Leu Lys Glu Ala Tyr Arg Met Tyr Thr
        355                 360                 365

Pro Tyr Asp Pro Glu Asp Pro Gly Gln Ala Ala Ser Val Ile Leu Ser
    370                 375                 380

Phe Ile Tyr Gln Ser Ser Pro Asp Ile Arg Asn Lys Leu Gln Arg Leu
385                 390                 395                 400
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Glu Gly Leu Gln Gly Phe Thr Leu Ser Asp Leu Leu Lys Glu Ala Glu
                405                 410                 415

Lys Ile Tyr Asn Lys Arg Glu Thr Pro Glu Glu Arg Glu Glu Arg Leu
            420                 425                 430

Trp Gln Arg Gln Glu Glu Arg Asp Lys Lys Arg His Lys Glu Met Thr
        435                 440                 445

Lys Val Leu Ala Thr Val Val Ala Gln Asn Arg Asp Lys Asp Arg Gly
    450                 455                 460

Glu Ser Lys Leu Gly Asp Gln Arg Lys Ile Pro Leu Gly Lys Asp Gln
465                 470                 475                 480

Cys Ala Tyr Cys Lys Glu Lys Gly His Trp Val Arg Asp Cys Pro Lys
                485                 490                 495

Arg Pro Arg Lys Lys Pro Ala Asn Ser Thr Leu Leu
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<210> 5
<211> 1530
<212> DNA
<213> Feline leukemia virus

<220>
<221> misc_feature
<222> (1)..(1530)
<223> DNA sequence of the mutagenized "gag" gene

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atcagccagg tggaggagag gatcttcgcc cccggccccc acggccaccc cgaccagatc 240

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<210> 6
<211> 509
<212> PRT
<213> Feline leukemia virus

<220>
<221> PEPTIDE
<222> (1)..(509)
<223> Amino acid sequence of the protein corresponding to Seq.ID5

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20 25 30

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Lys Lys Trp Ile Thr Leu Cys Glu Ala Glu Trp Val Met Met Asn Val
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Gly Trp Pro Arg Glu Gly Thr Phe Thr Ile Asp Asn Ile Ser Gln Val
    50                  55                  60

Glu Glu Arg Ile Phe Ala Pro Gly Pro Tyr Gly His Pro Asp Gln Ile
65                  70                  75                  80

Pro Tyr Ile Thr Thr Trp Arg Ser Leu Ala Thr Asp Pro Pro Pro Trp
                85                  90                  95

Val Arg Pro Phe Leu Pro Pro Pro Lys His Pro Arg Thr Asp Pro Pro
            100                 105                 110

Glu Pro Leu Ser Pro Gln Pro Leu Ala Pro Gln Pro Ser Ala Pro Pro
        115                 120                 125

Ile Ser Ser Leu Tyr Pro Val Leu Pro Lys Pro Asp Pro Pro Lys Ala
    130                 135                 140

Pro Val Leu Pro Pro Asn Pro Ser Ser Pro Leu Ile Asp Leu Leu Thr
145                 150                 155                 160

Glu Glu Pro Pro Pro Tyr Pro Gly Gly His Gly Pro Thr Pro Pro Ser
                165                 170                 175

Gly Pro Arg Thr Pro Thr Ala Ser Pro Ile Ala Ser Arg Leu Arg Glu
            180                 185                 190

Arg Arg Glu Asn Pro Ala Glu Lys Ser Gln Ala Leu Pro Leu Arg Glu
        195                 200                 205

Asp Pro Asn Asn Arg Pro Gln Tyr Trp Pro Phe Ser Ala Ser Asp Leu
    210                 215                 220

Tyr Asn Trp Lys Leu His Asn Pro Pro Phe Ser Gln Asp Pro Val Ala
225                 230                 235                 240

Leu Thr Asn Leu Ile Glu Ser Ile Leu Val Thr His Gln Pro Thr Trp
                245                 250                 255

Asp Asp Cys Gln Gln Leu Leu Gln Ala Leu Leu Thr Ala Glu Glu Arg
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            260                 265                 270

Gln Arg Val Leu Leu Glu Ala Arg Lys Gln Val Pro Gly Glu Asp Gly
        275                 280                 285

Arg Pro Thr Gln Leu Pro Asn Val Val Asp Glu Ala Phe Pro Leu Thr
    290                 295                 300

Arg Pro Asn Trp Asp Phe Cys Thr Pro Ala Gly Arg Glu His Leu Arg
305                 310                 315                 320

Leu Tyr Arg Gln Leu Leu Leu Ala Gly Leu Arg Gly Ala Ala Arg Arg
                325                 330                 335

Pro Thr Asn Leu Ala Gln Val Lys Gln Val Val Gln Gly Lys Glu Glu
            340                 345                 350

Thr Pro Ala Ser Phe Leu Glu Arg Leu Lys Glu Ala Tyr Arg Met Tyr
        355                 360                 365

Thr Pro Tyr Asp Pro Glu Asp Pro Gly Gln Ala Thr Ser Val Ile Leu
    370                 375                 380

Ser Phe Ile Tyr Gln Ser Ser Pro Asp Ile Arg Asn Lys Leu Gln Arg
385                 390                 395                 400

Leu Glu Gly Leu Gln Gly Phe Thr Leu Ser Asp Leu Leu Lys Glu Ala
                405                 410                 415

Glu Lys Ile Tyr Asn Lys Arg Glu Thr Pro Glu Glu Arg Glu Glu Arg
            420                 425                 430

Leu Trp Gln Arg Gln Glu Glu Arg Asp Lys Lys Arg His Lys Glu Met
        435                 440                 445

Thr Lys Val Leu Ala Thr Val Val Ala Gln Asn Arg Asp Lys Asp Arg
    450                 455                 460

Gly Glu Ser Lys Leu Gly Asp Gln Arg Lys Ile Pro Leu Gly Lys Asp
465                 470                 475                 480

Gln Cys Ala Tyr Cys Lys Glu Lys Gly His Trp Val Arg Asp Cys Pro
                485                 490                 495
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Lys Arg Pro Arg Lys Lys Pro Ala Asn Ser Thr Leu Leu
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<210> 7
<211> 1929
<212> DNA
<213> Feline leukemia virus

<220>
<221> misc_feature
<222> (1)..(1929)
<223> DNA sequence for the mutagenized "env" gene (gp85)

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tctatgctgg gcaccctgac agatgcatac cccaccctgc atgtggacct gtgtgacctg 240

gtgggggaca cctgggagcc cattccgctg aaccccacca atgtgaagca tggggccagg 300

tactcctcct ccaagtatgg ctgcaagacc acagacagga agaagcagca gcagacctac 360

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ggggcccagg atggcttctg tgctgcctgg ggctgtgaaa ccacagggga ggcctggtgg 480

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ctgaatgcca cagaccccaa caagaccaag gactgctggc tgtgcctggt gtccaggccc 960

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cgaccatga 1929

<210> 8
<211> 1440
<212> DNA
<213> Feline leukemia virus

<220>
<221> misc_feature
<222> (1)..(1440)
<223> DNA Sequence of the mutagenized "env" gene (gp70)

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tctatgctgg gcaccctgac agatgcatac cccaccctgc atgtggacct gtgtgacctg 240

gtgggggaca cctgggagcc cattccgctg aaccccacca atgtgaagca tggggccagg 300

tactcctcct ccaagtatgg ctgcaagacc acagacagga agaagcagca gcagacctac 360

cccttctatg tgtgccctgg ccatgccccc tccctgggcc ccaagggcac ccactgtggg 420

ggggcccagg atggcttctg tgctgcctgg ggctgtgaaa ccacagggga ggcctggtgg 480

aagcccacct cctcctggga ctacatcaca gtgaagaggg gctcctccca ggacaactcc 540

tgtgagggca agtgcaaccc cctggtgctg cagttcaccc agaagggcag gcaggcctcc 600

tgggatggcc ccaagatgtg gggcctgagg ctgtacagga caggctatga ccccattgcc 660

ctgttcacag tgtccaggca ggtgtccacc atcaccccca cccaggccat gggccccaac 720

ctggtgctgc ctgaccagaa gccccctcc aggcagtccc agacaggctc caaggtggcc 780

acccagaggc cccagaccaa tgagtctgcc cccaggtctg tggcccccac caccatgggc 840

cccaagagga ttggcacagg ggacaggctg atcaacctgg tgcagggcac ctacctggcc 900

ctgaatgcca cagaccccaa caagaccaag gactgctggc tgtgcctggt gtccaggccc 960

ccctactatg agggcattgc catcctgggc aactactcca accagaccaa ccccccccc 1020

tcctgcctgt ccacccccca gcacaagctg accatctctg aggtgtctgg ccagggcatg 1080

tgcattggca cagtgcccaa gacccaccag gccctgtgca acaagaccca gcagggccac 1140

acaggggccc actacctggc tgtccccaat ggcacctact gggcctgcaa cacaggcctg 1200

acccccтgca tctccatggc tgtgctgaac tggacctctg acttctgtgt gctgattgag 1260

ctgtggccca gggtgaccta ccaccagcct gagtatgtgt acacccactt tgccaaggct 1320

gtgaggttca ggagggagcc catctccctg acagtggccc tgatgctggg gggcctgaca 1380

gtgggggca ttgctgctgg ggtgggcaca ggcaccaagg ccctgctgga aacagcctga 1440

<210> 9
<211> 642
<212> PRT
<213> Feline leukemia virus

<220>
<221> PEPTIDE
<222> (1)..(642)
<223> Amino acid sequence of the protein corresponding to Seq.ID7

<400> 9

Met Glu Ser Pro Thr His Pro Lys Pro Ser Lys Asp Lys Thr Leu Ser
1 5 10 15

Trp Asn Met Val Phe Leu Val Gly Ile Leu Phe Thr Ile Asp Ile Gly
20 25 30

Met Ala Asn Pro Ser Pro Pro Arg Ile Tyr Asn Val Thr Trp Val Ile
35 40 45

```
Thr Asn Val Gln Thr Asn Thr Gln Ala Asn Ala Thr Ser Met Leu Gly
    50                  55                  60

Thr Leu Thr Asp Ala Tyr Pro Thr Leu His Val Asp Leu Cys Asp Leu
65                  70                  75                  80

Val Gly Asp Thr Trp Glu Pro Ile Pro Leu Asn Pro Thr Asn Val Lys
                85                  90                  95

His Gly Ala Arg Tyr Ser Ser Ser Lys Tyr Gly Cys Lys Thr Thr Asp
            100                 105                 110

Arg Lys Lys Gln Gln Gln Thr Tyr Pro Phe Tyr Val Cys Pro Gly His
        115                 120                 125

Ala Pro Ser Leu Gly Pro Lys Gly Thr His Cys Gly Gly Ala Gln Asp
    130                 135                 140

Gly Phe Cys Ala Ala Trp Gly Cys Glu Thr Thr Gly Glu Ala Trp Trp
145                 150                 155                 160

Lys Pro Thr Ser Ser Trp Asp Tyr Ile Thr Val Lys Arg Gly Ser Ser
                165                 170                 175

Gln Asp Asn Ser Cys Glu Gly Lys Cys Asn Pro Leu Val Leu Gln Phe
            180                 185                 190

Thr Gln Lys Gly Arg Gln Ala Ser Trp Asp Gly Pro Lys Met Trp Gly
        195                 200                 205

Leu Arg Leu Tyr Arg Thr Gly Tyr Asp Pro Ile Ala Leu Phe Thr Val
    210                 215                 220

Ser Arg Gln Val Ser Thr Ile Thr Pro Pro Gln Ala Met Gly Pro Asn
225                 230                 235                 240

Leu Val Leu Pro Asp Gln Lys Pro Pro Ser Arg Gln Ser Gln Thr Gly
                245                 250                 255

Ser Lys Val Ala Thr Gln Arg Pro Gln Thr Asn Glu Ser Ala Pro Arg
            260                 265                 270

Ser Val Ala Pro Thr Thr Met Gly Pro Lys Arg Ile Gly Thr Gly Asp
```

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        275                 280                 285

Arg Leu Ile Asn Leu Val Gln Gly Thr Tyr Leu Ala Leu Asn Ala Thr
    290                 295                 300

Asp Pro Asn Lys Thr Lys Asp Cys Trp Leu Cys Leu Val Ser Arg Pro
305                 310                 315                 320

Pro Tyr Tyr Glu Gly Ile Ala Ile Leu Gly Asn Tyr Ser Asn Gln Thr
                325                 330                 335

Asn Pro Pro Pro Ser Cys Leu Ser Thr Pro Gln His Lys Leu Thr Ile
            340                 345                 350

Ser Glu Val Ser Gly Gln Gly Met Cys Ile Gly Thr Val Pro Lys Thr
        355                 360                 365

His Gln Ala Leu Cys Asn Lys Thr Gln Gln Gly His Thr Gly Ala His
    370                 375                 380

Tyr Leu Ala Val Pro Asn Gly Thr Tyr Trp Ala Cys Asn Thr Gly Leu
385                 390                 395                 400

Thr Pro Cys Ile Ser Met Ala Val Leu Asn Trp Thr Ser Asp Phe Cys
                405                 410                 415

Val Leu Ile Glu Leu Trp Pro Arg Val Thr Tyr His Gln Pro Glu Tyr
            420                 425                 430

Val Tyr Thr His Phe Ala Lys Ala Val Arg Phe Arg Arg Glu Pro Ile
        435                 440                 445

Ser Leu Thr Val Ala Leu Met Leu Gly Gly Leu Thr Val Gly Gly Ile
    450                 455                 460

Ala Ala Gly Val Gly Thr Gly Thr Lys Ala Leu Leu Glu Thr Ala Gln
465                 470                 475                 480

Phe Arg Gln Leu Gln Met Ala Met His Thr Asp Ile Gln Ala Leu Glu
                485                 490                 495

Glu Ser Val Ser Ala Leu Glu Lys Ser Leu Thr Ser Leu Ser Glu Val
            500                 505                 510
```

```
Val Leu Gln Asn Arg Arg Gly Leu Asp Ile Leu Phe Leu Gln Glu Gly
        515                 520                 525

Gly Leu Cys Ala Ala Leu Lys Glu Glu Cys Cys Phe Tyr Ala Asp His
    530                 535                 540

Thr Gly Leu Val Arg Asp Asn Met Ala Lys Leu Arg Glu Arg Leu Lys
545                 550                 555                 560

Gln Arg Gln Gln Leu Phe Asp Ser Gln Gln Gly Trp Phe Glu Gly Trp
                565                 570                 575

Phe Asn Lys Ser Pro Trp Leu Thr Thr Leu Ile Ser Ser Ile Met Gly
            580                 585                 590

Pro Leu Leu Ile Leu Leu Leu Leu Ile Leu Leu Phe Gly Pro Cys Ile Leu
        595                 600                 605

Asn Arg Leu Val Gln Phe Val Lys Asp Arg Ile Ser Val Val Gln Ala
    610                 615                 620

Leu Val Leu Thr Gln Gln Tyr Gln Gln Ile Lys Gln Tyr Asp Pro Asp
625                 630                 635                 640

Arg Pro
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<210> 10
<211> 479
<212> PRT
<213> Feline leukemia virus

<220>
<221> PEPTIDE
<222> (1)..(479)
<223> Amino acid sequence of the protein corresponding to Seq.ID8

<400> 10

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Met Glu Ser Pro Thr His Pro Lys Pro Ser Lys Asp Lys Thr Leu Ser
1               5                   10                  15

Trp Asn Met Val Phe Leu Val Gly Ile Leu Phe Thr Ile Asp Ile Gly
            20                  25                  30
```

```
Met Ala Asn Pro Ser Pro Pro Arg Ile Tyr Asn Val Thr Trp Val Ile
        35                  40                  45

Thr Asn Val Gln Thr Asn Thr Gln Ala Asn Ala Thr Ser Met Leu Gly
    50                  55                  60

Thr Leu Thr Asp Ala Tyr Pro Thr Leu His Val Asp Leu Cys Asp Leu
65                  70                  75                  80

Val Gly Asp Thr Trp Glu Pro Ile Pro Leu Asn Pro Thr Asn Val Lys
                85                  90                  95

His Gly Ala Arg Tyr Ser Ser Ser Lys Tyr Gly Cys Lys Thr Thr Asp
            100                 105                 110

Arg Lys Lys Gln Gln Gln Thr Tyr Pro Phe Tyr Val Cys Pro Gly His
        115                 120                 125

Ala Pro Ser Leu Gly Pro Lys Gly Thr His Cys Gly Gly Ala Gln Asp
    130                 135                 140

Gly Phe Cys Ala Ala Trp Gly Cys Glu Thr Thr Gly Glu Ala Trp Trp
145                 150                 155                 160

Lys Pro Thr Ser Ser Trp Asp Tyr Ile Thr Val Lys Arg Gly Ser Ser
                165                 170                 175

Gln Asp Asn Ser Cys Glu Gly Lys Cys Asn Pro Leu Val Leu Gln Phe
            180                 185                 190

Thr Gln Lys Gly Arg Gln Ala Ser Trp Asp Gly Pro Lys Met Trp Gly
        195                 200                 205

Leu Arg Leu Tyr Arg Thr Gly Tyr Asp Pro Ile Ala Leu Phe Thr Val
    210                 215                 220

Ser Arg Gln Val Ser Thr Ile Thr Pro Pro Gln Ala Met Gly Pro Asn
225                 230                 235                 240

Leu Val Leu Pro Asp Gln Lys Pro Pro Ser Arg Gln Ser Gln Thr Gly
                245                 250                 255
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```
Ser Lys Val Ala Thr Gln Arg Pro Gln Thr Asn Glu Ser Ala Pro Arg
            260                 265                 270

Ser Val Ala Pro Thr Thr Met Gly Pro Lys Arg Ile Gly Thr Gly Asp
        275                 280                 285

Arg Leu Ile Asn Leu Val Gln Gly Thr Tyr Leu Ala Leu Asn Ala Thr
    290                 295                 300

Asp Pro Asn Lys Thr Lys Asp Cys Trp Leu Cys Leu Val Ser Arg Pro
305                 310                 315                 320

Pro Tyr Tyr Glu Gly Ile Ala Ile Leu Gly Asn Tyr Ser Asn Gln Thr
                325                 330                 335

Asn Pro Pro Pro Ser Cys Leu Ser Thr Pro Gln His Lys Leu Thr Ile
            340                 345                 350

Ser Glu Val Ser Gly Gln Gly Met Cys Ile Gly Thr Val Pro Lys Thr
        355                 360                 365

His Gln Ala Leu Cys Asn Lys Thr Gln Gln Gly His Thr Gly Ala His
    370                 375                 380

Tyr Leu Ala Val Pro Asn Gly Thr Tyr Trp Ala Cys Asn Thr Gly Leu
385                 390                 395                 400

Thr Pro Cys Ile Ser Met Ala Val Leu Asn Trp Thr Ser Asp Phe Cys
                405                 410                 415

Val Leu Ile Glu Leu Trp Pro Arg Val Thr Tyr His Gln Pro Glu Tyr
            420                 425                 430

Val Tyr Thr His Phe Ala Lys Ala Val Arg Phe Arg Arg Glu Pro Ile
        435                 440                 445

Ser Leu Thr Val Ala Leu Met Leu Gly Gly Leu Thr Val Gly Gly Ile
    450                 455                 460

Ala Ala Gly Val Gly Thr Gly Thr Lys Ala Leu Leu Glu Thr Ala
465                 470                 475
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<210> 11
<211> 1440
<212> DNA
<213> Feline leukemia virus

<220>
<221> gene
<222> (1)..(1440)
<223> DNA sequence of wildtype "env" gene (gp70)

<400> 11
atggaaaqtc caacgcaccc aaaaccctct aaagataaga ctctctcgtg gaacttagcg 60

tttctggtgg ggatcttatt tacaatagac ataggaatgg ccaatcctag tccacaccaa 120

atatataatg taacttgggt aataaccaat gtacaaacta acacccaagc taacgccacc 180

tctatgttag gaaccttaac cgatgcctac cctaccctac atgttgactt atgtgaccta 240

gtgggagaca cctgggaacc tatagtccta aacccaacca atgtaaaaca cggggcacgt 300

tactcctcct caaaatatgg atgtaaaact acagatagaa aaaaacagca acagacatac 360

ccctttacg tctgccccgg acatgccccc tcgttggggc caaagggaac acattgtgga 420

ggggcacaag atgggttttg tgccgcatgg ggatgtgaga ccaccggaga agcttggtgg 480

aagcccacct cctcatggga ctatatcaca gtaaaaagag ggagtagtca ggacaatagc 540

tgtgagggaa aatgcaaccc cctggttttg cagttcaccc agaagggaag acaagcctct 600

tgggacggac ctaagatgtg gggattgcga ctataccgta caggatatga ccctatcgct 660

ttattcacgg tgtcccggca ggtatcaacc attacgccgc ctcaggcaat gggaccaaac 720

ctagtcttac ctgatcaaaa acccccatcc cgacaatctc aaacagggtc caaagtggcg 780

acccagaggc cccaaacgaa tgaaagcgcc ccaaggtctg ttgcccccac caccatgggt 840

cccaaacgga ttgggaccgg agataggtta ataaatttag tacaagggac atacctagcc 900

ttaaatgcca ccgaccccaa caaaactaaa gactgttggc tctgcctggt ttctcgacca 960

ccctattacg aagggattgc aatcttaggt aactacagca accaaacaaa ccccccccca 1020

tcctgcctat ctactccgca acacaaacta actatatctg aagtatcagg gcaaggaatg 1080

tgcataggga ctgttcctaa aacccaccag gctttgtgca ataagacaca acagggacat 1140

acaggggcgc actatctagc cgcccccaac ggcacctatt gggcctgtaa cactggactc 1200

accccatgca tttccatggc ggtgctcaat tggacctctg atttttgtgt cttaatcgaa 1260

ttatggccca gagtgactta ccatcaaccc gaatatgtgt acacacattt tgccaaagct 1320

gtcaggttcc gaagagaacc aatatcacta acggttgccc ttatgttggg aggacttact 1380

gtaggggca tagccgcggg ggtcggaaca gggactaaag ccctccttga aacagcctga 1440

<210> 12
<211> 42
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(42)
<223> gag-mut1-rneu

<400> 12
aattaagagc tccacgtctc cccccgctaa cagcaactgg cg 42

<210> 13
<211> 45
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(45)
<223> gag-mut2-1

<400> 13
aattaagagc tccaggtctc cggggctccg cggggctgca agacg 45

<210> 14
<211> 48
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(48)
<223> gag-mut3-r

<400> 14
aattaagagc tccacgtctc cttccctttt gttgtatatc ttttctgc 48

<210> 15
<211> 48
<212> DNA
<213> Primer

<220>
<221> misc_feature

<222> (1)..(48)
<223> gag-mut4-1

<400> 15
aattaagagc tccaggtctc cggaaacccc agaggaaagg gaagaaag 48

<210> 16
<211> 34
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(34)
<223> Felvgag-1

<400> 16
cggataaggt accatgggcc aaactataac tacc 34

<210> 17
<211> 37
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(37)
<223> Felvgag-r

<400> 17
ttctcagagc tcttagagga gagtggagtt ggcgggt 37

<210> 18
<211> 33
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(33)
<223> env1

<400> 18
cggataaggt accatggcca atcctagtcc acc 33

<210> 19
<211> 37
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(37)
<223> envr

<400> 19
agttctcaga gctcttaggc tgtttcaagg agggctt 37

<210> 20
<211> 28
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(28)
<223> Primer

<400> 20
atattggatc ccatggccaa cccctccc 28

<210> 21
<211> 34
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(34)
<223> Primer

<400> 21
attatggtct cctgctgctt cttcctgtct gtgg 34

<210> 22
<211> 30
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(30)
<223> Primer

<400> 22
taataggtct ccagcagcag acctacccct 30

<210> 23
<211> 33

<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(33)
<223> Primer

<400> 23
taataggtct ctgtgaacag ggcaatgggg tca 33

<210> 24
<211> 34
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(34)
<223> Primer

<400> 24
tatttggtct cttcacagtg tccaggcagg tgtc 34

<210> 25
<211> 30
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(30)
<223> Primer

<400> 25
tattaggtct cagcttgtgc tgggggtgg 30

<210> 26
<211> 34
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(34)
<223> Primer

<400> 26
aataaggtct ccaagctgac catctctgag gtgt 34

<210> 27
<211> 27
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(27)
<223> Primer

<400> 27
attaagagct ctcaggctgt ttccagc 27

<210> 28
<211> 31
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(31)
<223> Primer

<400> 28
attgccggta ccatggagtc ccccacccac c 31

<210> 29
<211> 35
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(35)
<223> Primer

<400> 29
atcagaggtc tcccatgcca atgtcaatgg tgaac 35

<210> 30
<211> 27
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(27)
<223> Primer

<400> 30
gatctgggtc tccatggcca acccctc 27

<210> 31
<211> 36
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(36)
<223> Primer

<400> 31
aattatggtc tcgcagttca gacaactaca aatggc 36

<210> 32
<211> 30
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(30)
<223> Primer

<400> 32
aattatgagc tctcagggcc tgtcagggtc 30

<210> 33
<211> 28
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(28)
<223> Primer

<400> 33
aattatggta ccatggagtc ccccaccc 28

<210> 34
<211> 35
<212> DNA
<213> Primer

<220>
<221> misc_feature

<222> (1)..(35)
<223> Primer

<400> 34
tataatggtc tcaactgggc tgtttccagc agggc 35

<210> 35
<211> 31
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(31)
<223> Primer

<400> 35
atattaggtc tcagatccgg gggggggagg g 31

<210> 36
<211> 30
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(30)
<223> Primer

<400> 36
atattggtct caggagaggg acaagaagag 30

<210> 37
<211> 32
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(32)
<223> Primer

<400> 37
aatatggtct ctcagcctgc tggcgatggg gc 32

<210> 38
<211> 32
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(32)
<223> Primer

<400> 38
attatggtct ctgcacctga ggctgtacag gc 32

<210> 39
<211> 36
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(36)
<223> Primer

<400> 39
aatatggtct cggtgctccc tgccggcggg ggtgca 36

<210> 40
<211> 28
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(28)
<223> Primer

<400> 40
aatatggtct ctctcctcct gcctctgc 28

<220> 41
<211> 7
<212> PRT
<213> SV40

<220>
<221> peptide
<222>(1)..(7)
<223> Nuclear Localization Signal from SV40

<400> 41
Pro Lys Lys Lys Arg Lys Val
1 5